



1/16

#4

SEQUENCE LISTING

<110> Huang, Qian
Richmond, Joan F.L.
Cho, Bryan K.
Palliser, Deborah
Chen, Jianzhu
Eisen, Herman N.
Young, Richard A.

<120> In Vivo CTL Elicitation By Heat Shock
Protein Fusion Proteins Maps To A Discrete Domain and is
CD4+T Cell-Independent

<130> 0399.2006-003

<140> US 09/761,534

<141> 2001-01-16

<150> PCT/US00/32831

<151> 2000-12-01

<150> US 60/176,143

<151> 2000-01-14

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 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
 20 25 30
 tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt gag gtg 144
 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
 35 40 45
 ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc gat cgc 192
 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
 50 55 60
 acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc ata gag 240
 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
 65 70 75 80

att gac ggc aag aaa tac acc gcg ccg gag atc agc gcc cgc att ctg	288
Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu	
85 90 95	
atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac att acc	336
Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr	
100 105 110	
gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag cgt cag	384
Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln	
115 120 125	
gcc acc aag gac gcc ggc cag atc gcc ggc ctc aac gtg ctg cgg atc	432
Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile	
130 135 140	
gtc aac gag ccg acc gcg gcc gcg ctg gcc tac ggc ctc gac aag ggc	480
Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly	
145 150 155 160	
gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc act ttc	528
Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe	
165 170 175	
gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc	576
Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala	
180 185 190	
act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc	624
Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val	
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Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu	
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Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys	
225 230 235 240	
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Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro	
245 250 255	
tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag	816
Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln	
260 265 270	
ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc	864
Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg	
275 280 285	
act cgc aag ccg ttc cag tcg gtg atc gct gac acc ggc att tcg gtg	912
Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val	
290 295 300	

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Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
325                      330                      335

aag ggc gtc aac ccc gat gag gtt gtc gcg gtg gga gcc gct ctg cag 1056
Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
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Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
355                      360                      365

acc ccg ctg agc ctg ggt atc gag acc aag ggc ggg gtg atg acc agg 1152
Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
370                      375                      380

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Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
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35     40     45
Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
50     55     60
Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
65     70     75     80
Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
85     90     95
Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
100    105    110
Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
115    120    125
Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
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Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
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 165 170 175
 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
 180 185 190
 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
 195 200 205
 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
 245 250 255
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 260 265 270
 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
 275 280 285
 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
 290 295 300
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 305 310 315 320
 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
 340 345 350
 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
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 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
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Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val	
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Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu	
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Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys	
65 70 75 80	
gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc	288
Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro	
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Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln	
100 105 110	
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Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg	
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Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro	
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Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn	
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Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln	
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gcc ggc gtc ctc aag ggc gag gtg aaa gac gtt ctg ctg ctt gat gtt	624
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 35 40 45
 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
 50 55 60
 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
 65 70 75 80
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
 85 90 95
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 100 105 110
 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
 115 120 125
 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
 130 135 140
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 145 150 155 160
 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
 165 170 175
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 Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile Ile Ala Asn Asp
 20 25 30
 cag ggc aac cgc acg acc ccc agc tac gtg gcc ttc acc gac acc gag 144
 Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr Asp Thr Glu
 35 40 45

cgc ctc atc ggg gac gcc gcc aag aac cag gtg gcg ctg aac ccg cag	192
Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Leu Asn Pro Gln	
50 55 60	
aac acc gtg ttc gac gcg aag cgg ctg atc ggc cgc aag ttc ggc gat	240
Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Lys Phe Gly Asp	
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Ala Val Val Gln Ser Asp Met Lys His Trp Pro Phe Gln Val Val Asn	
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gac ggc gac aag ccc aag gtg cag gtg aac tac aag ggc gag agc cgg	336
Asp Gly Asp Lys Pro Lys Val Gln Val Asn Tyr Lys Gly Glu Ser Arg	
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tcg ttc ttc ccg gag gag atc tcg tcc atg gtg ctg acg aag atg aag	384
Ser Phe Phe Pro Glu Glu Ile Ser Ser Met Val Leu Thr Lys Met Lys	
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gag atc gct gag gcg tac ctg ggc cac ccg gtg acc aac gcg gtg atc	432
Glu Ile Ala Glu Ala Tyr Leu Gly His Pro Val Thr Asn Ala Val Ile	
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acg gtg ccc gcc tac ttc aac gac tct cag cgg cag gcc acc aag gac	480
Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp	
145 150 155 160	
gcg ggc gtg atc gcc ggt cta aac gtg ctg cgg atc atc aac gag ccc	528
Ala Gly Val Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro	
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Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Arg Thr Gly Lys Gly Glu	
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Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala Thr Ala Gly	
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Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile Ser Gln Asn	
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Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu	
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Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val Glu Lys Ala	
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Asn Ser Thr Ile Pro Thr Lys Gln Thr Gln Thr Phe Thr Thr Tyr Ser	
420 425 430	
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Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu Gly Glu Arg Ala	
435 440 445	
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Met Thr Arg Asp Asn Asn Leu Leu Gly Arg Phe Glu Leu Ser Gly Ile	
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Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile	
465 470 475 480	
gac gcc aac ggc atc ctg aac gtc acg gcc acc gac aag agc acc ggc	1488
Asp Ala Asn Gly Ile Leu Asn Val Thr Ala Thr Asp Lys Ser Thr Gly	
485 490 495	

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Lys Ala Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys	
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Glu Glu Ile Glu Arg Met Val Gln Glu Ala Glu Arg Tyr Lys Ala Glu	
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Asp Glu Val Gln Arg Asp Arg Val Ala Ala Lys Asn Ala Leu Glu Ser	
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Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly	
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Lys Leu Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu	
565 570 575	
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Val Ile Ser Trp Leu Asp Ser Asn Thr Leu Ala Asp Lys Glu Glu Phe	
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Val His Lys Arg Glu Glu Leu Glu Arg Val Cys Ser Pro Ile Ile Ser	
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 35 40 45
 Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Leu Asn Pro Gln
 50 55 60

Asn	Thr	Val	Phe	Asp	Ala	Lys	Arg	Leu	Ile	Gly	Arg	Lys	Phe	Gly	Asp
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Ala	Val	Val	Gln	Ser	Asp	Met	Lys	His	Trp	Pro	Phe	Gln	Val	Val	Asn
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Asp	Gly	Asp	Lys	Pro	Lys	Val	Gln	Val	Asn	Tyr	Lys	Gly	Glu	Ser	Arg
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225					230					235					240
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Lys	Arg	Ala	Val	Arg	Arg	Leu	Arg	Thr	Ala	Cys	Glu	Arg	Ala	Lys	Arg
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Leu	Gly	Leu	Glu	Thr	Ala	Gly	Gly	Val	Met	Thr	Ala	Leu	Ile	Lys	Arg
				405					410					415	
Asn	Ser	Thr	Ile	Pro	Thr	Lys	Gln	Thr	Gln	Thr	Phe	Thr	Thr	Tyr	Ser
			420					425					430		
Asp	Asn	Gln	Pro	Gly	Val	Leu	Ile	Gln	Val	Tyr	Glu	Gly	Glu	Arg	Ala
		435					440					445			
Met	Thr	Arg	Asp	Asn	Asn	Leu	Leu	Gly	Arg	Phe	Glu	Leu	Ser	Gly	Ile
	450					455					460				
Pro	Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile
465					470					475					480
Asp	Ala	Asn	Gly	Ile	Leu	Asn	Val	Thr	Ala	Thr	Asp	Lys	Ser	Thr	Gly
				485					490					495	
Lys	Ala	Asn	Lys	Ile	Thr	Ile	Thr	Asn	Asp	Lys	Gly	Arg	Leu	Ser	Lys
		500						505					510		
Glu	Glu	Ile	Glu	Arg	Met	Val	Gln	Glu	Ala	Glu	Arg	Tyr	Lys	Ala	Glu
		515					520						525		

Asp Glu Val Gln Arg Asp Arg Val Ala Ala Lys Asn Ala Leu Glu Ser
 530 535 540
 Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly
 545 550 555 560
 Lys Leu Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu
 565 570 575
 Val Ile Ser Trp Leu Asp Ser Asn Thr Leu Ala Asp Lys Glu Glu Phe
 580 585 590
 Val His Lys Arg Glu Glu Leu Glu Arg Val Cys Ser Pro Ile Ile Ser
 595 600 605
 Gly Leu Tyr Gln Gly Ala Gly Ala Pro Gly Ala Gly Gly Phe Gly Ala
 610 615 620
 Gln Ala Pro Pro Lys Gly Ala Ser Gly Ser Gly Pro Thr Ile Glu Glu
 625 630 635 640
 Val Asp

<210> 11
 <211> 627
 <212> DNA
 <213> Unknown

<220>
 <223> Murine hsp70 -Segment II
 <221> CDS
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 <223> Murine hsp70 -Segment II

<400> 11
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 Lys Gly Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe
 1 5 10 15
 gac gtg tcc atc ctg acg atc gac gac ggc atc ttc gag gtg aag gcc 96
 Asp Val Ser Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala
 20 25 30
 acg gcg ggc gac acg cac ctg gga ggg gag gac ttc gac aac cgg ctg 144
 Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu
 35 40 45
 gtg agc cac ttc gtg gag gag ttc aag agg aag cac aag aag gac atc 192
 Val Ser His Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile
 50 55 60
 agc cag aac aag cgc gcg gtg cgg cgg ctg cgc acg gcg tgt gag agg 240
 Ser Gln Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg
 65 70 75 80
 gcc aag agg acg ctg tcg tcc agc acc cag gcc agc ctg gag atc gac 288
 Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp
 85 90 95
 tct ctg ttc gag ggc atc gac ttc tac aca tcc atc acg cgg gcg cgg 336
 Ser Leu Phe Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg
 100 105 110

ttc gaa gag ctg tgc tgc gac ctg ttc cgc ggc acg ctg gag ccc gtg	384
Phe Glu Glu Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val	
115 120 125	
gag aag gcc ctg cgc gac gcc aag atg gac aag gcc cag atc cac gac	432
Glu Lys Ala Leu Arg Asp Ala Lys Met Asp Lys Ala Gln Ile His Asp	
130 135 140	
ctg gtg ctg gtg ggc ggc tgc acg cgc atc ccc aag gtg cag aag ctg	480
Leu Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Leu	
145 150 155 160	
ctg cag gac ttc ttc aac ggg cgc gac ctg aac aag agc atc aac ccg	528
Leu Gln Asp Phe Phe Asn Gly Arg Asp Leu Asn Lys Ser Ile Asn Pro	
165 170 175	
gac gag gcg gtg gcc tac ggg gcg gcg gtg cag gcg gcc atc ctg atg	576
Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu Met	
180 185 190	
ggg gac aag tgc gag aac gtg cag gac ctg ctg ctg ctg gac gtg gcg	624
Gly Asp Lys Ser Glu Asn Val Gln Asp Leu Leu Leu Leu Asp Val Ala	
195 200 205	
ccc	627
Pro	

<210> 12
 <211> 209
 <212> PRT
 <213> Unknown

<220>
 <223> Murine hsp70 - Segment II

<400> 12

Lys Gly Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe	
1 5 10 15	
Asp Val Ser Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala	
20 25 30	
Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu	
35 40 45	
Val Ser His Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile	
50 55 60	
Ser Gln Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg	
65 70 75 80	
Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp	
85 90 95	
Ser Leu Phe Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg	
100 105 110	
Phe Glu Glu Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val	
115 120 125	
Glu Lys Ala Leu Arg Asp Ala Lys Met Asp Lys Ala Gln Ile His Asp	
130 135 140	
Leu Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Leu	
145 150 155 160	

Leu	Gln	Asp	Phe	Phe	Asn	Gly	Arg	Asp	Leu	Asn	Lys	Ser	Ile	Asn	Pro
				165					170					175	
Asp	Glu	Ala	Val	Ala	Tyr	Gly	Ala	Ala	Val	Gln	Ala	Ala	Ile	Leu	Met
			180					185					190		
Gly	Asp	Lys	Ser	Glu	Asn	Val	Gln	Asp	Leu	Leu	Leu	Leu	Asp	Val	Ala
		195					200					205			

Pro

<210> 13
 <211> 47
 <212> DNA
 <213> Unknown

<220>
 <223> PCR Primer

<400> 13
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<210> 14
 <211> 63
 <212> DNA
 <213> Unknown

<220>
 <223> PCR Primer

<400> 14
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 agt 63

<210> 15
 <211> 44
 <212> DNA
 <213> Unknown

<220>
 <223> PCR Primer

<400> 15
 atagtactgg atccatggct cgtgcggtcg ggatcgacct cggg 44

<210> 16
 <211> 36
 <212> DNA
 <213> Unknown

<400> 16
 ggaattccta tctagtcact tgccctcccg gccgtc 36

<210> 17
 <211> 49
 <212> DNA
 <213> Unknown

<220>
<223> PCR Primer

<400> 17
gtcgacgaat tcatcatcag attcgctgct cttctcgcc cttgtcgag 49

<210> 18
<211> 48
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 18
gtcgacggat ccatggagaa ggagcagcga atcctggctt tcgacttg 48

<210> 19
<211> 48
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 19
gtcgacggat ccatggtgaa agacgttctg ctgcttgatg ttaccccg 48

<210> 20
<211> 48
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 20
gtcgacggat ccatgcgtaa tcaagccgag acattggctt accagacg 48

<210> 21
<211> 49
<212> DNA
<213> Unknown

<220>
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<400> 21
gtcgacgaat tcatcacggg gtaacatcaa gcagcagaac gtctttcac 49

<210> 22
<211> 49
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 22
gtcgacgaat tcatcagacc aatgtctcgg cttgattacg aacatcggc 49

<210> 23
<211> 33
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 23
tctagaggat ccatggccaa gaacacggcg atc 33

<210> 24
<211> 39
<212> DNA
<213> Unknown

<220>
<223> PCR Primer

<400> 24
tctagagaat tcctaattcca cctcctcgat ggtgggtcc 39

<210> 25
<211> 24
<212> PRT
<213> Unknown

<220>
<223> P1 Peptide

<400> 25
Ile Lys Val Ser Gly Leu Glu Gln Leu Glu Ser Ile Tyr Arg Tyr Tyr
1 5 10 15
Gly Leu Leu Leu Lys Glu Ala Tyr
20